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 Harris, Curtis C.
 Nagashima, Makoto
 Shiseki, Masayuki
 Pedoux, Remy

<120> NEW TUMOR SUPPRESSOR GENE, p28ING5

<130> 4239-64141-02

<140> 10502431

<141> 2004-07-22

<150> PCT/US03/02174

<151> 2003-01-23

<150> 60/351,504

<151> 2002-01-23

<160> 6

<170> PatentIn version 3.5

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<211> 1068

<212> DNA

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Asn Leu Pro Cys Glu Leu Gln Arg Asn Phe Gln Leu Met Arg Glu Leu

20 25 30

gac cag agg acg gaa gat aag aaa gca gag att gac atc ctg gct gca 143

Asp Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu Ala Ala

35 40 45

gag tac atc tcc acg gtg aag acg ctg tct cca gac cag cgc gtg gag 191

Glu Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg Val Glu

50 55 60

cgc ctg cag aag atc cag aac gcc tac agc aag tgc aag gaa tac agt 239

Arg Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu Tyr Ser

65 70 75

gac gac aaa gtg cag ctg gcc atg cag acc tac gag atg gtg gat aaa	287
Asp Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val Asp Lys	
80 85 90 95	
 cac att cga agg ctt gat gca gac ctg gcg cgc ttt gaa gca gat ctg	335
His Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala Asp Leu	
100 105 110	
 aag gac aag atg gag ggc agt gat ttt gaa agc tcc gga ggg cga ggg	383
Lys Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly Arg Gly	
115 120 125	
 tta aaa aaa ggc cgg ggt cag aaa gaa aaa aga ggg tcc cgg ggc cga	431
Leu Lys Lys Gly Arg Gly Gln Lys Glu Lys Arg Gly Ser Arg Gly Arg	
130 135 140	
 ggc agg agg aca tca gag gaa gac aca cca aag aaa aag aag cac aaa	479
Gly Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys His Lys	
145 150 155	
 gga ggg tct gag ttc act gac acc atc ctg tcc gtg cac ccc tct gat	527
Gly Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro Ser Asp	
160 165 170 175	
 gtg ctg gac atg ccc gtg gac cca aac gaa ccc acg tac tgc ctg tgc	575
Val Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys	
180 185 190	
 cac cag gtc tcc tat ggg gag atg att ggc tgt gac aat cca gac tgt	623
His Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro Asp Cys	
195 200 205	
 cca att gag tgg ttt cac ttt gcc tgc gtg gac ctt acc acg aaa ccc	671
Pro Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr Lys Pro	
210 215 220	
 aaa gga aaa tgg ttc tgt cca cgg tgt gtc cag gaa aag agg aag aag	719
Lys Gly Lys Trp Phe Cys Pro Arg Cys Val Gln Glu Lys Arg Lys Lys	
225 230 235	
 aag tag gaggagctgt gtgcccggat ccgaggagca agttaatctg tcccttcatt	775
Lys	
240	
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cgtggccagt tgaagcgctg gatgtttcct agaacaagaa ccaccaaagc ctgttcgcac	895
agaagggcga ccttgcaggg actcgccgcc gcgacctcag tgtggctttt acaggactcc	955
ccccgagcat cagcagggac cccggcggac gtgggcgggc gcgcgtgagc tcgggctgcc	1015
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<213> Homo sapiens

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35 40 45

Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg Val Glu Arg
50 55 60

Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu Tyr Ser Asp
65 70 75 80

Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val Asp Lys His
85 90 95

Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala Asp Leu Lys
100 105 110

Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly Arg Gly Leu
115 120 125

Lys Lys Gly Arg Gly Gln Lys Glu Lys Arg Gly Ser Arg Gly Arg Gly
130 135 140

Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys His Lys Gly
145 150 155 160

Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro Ser Asp Val
165 170 175

Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys His
180 185 190

Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro Asp Cys Pro
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Gly Lys Trp Phe Cys Pro Arg Cys Val Gln Glu Lys Arg Lys Lys Lys
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35 40 45

Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
50 55 60

Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
65 70 75 80

Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
85 90 95

Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
100 105 110

Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Ala Gly Asn Ser Gly Lys
115 120 125

Ala Gly Ala Asp Arg Pro Lys Gly Glu Ala Ala Ala Gln Ala Asp Lys
130 135 140

Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
145 150 155 160

Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
165 170 175

Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
180 185 190

Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
195 200 205

Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
210 215 220

Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
225 230 235 240

Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
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Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
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Lys Glu Arg Ala Tyr Asn Arg
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Glu Cys Val Glu Ser Leu Pro His Asp Met Gln Arg Asn Val Ser Val
35 40 45

Leu Arg Glu Leu Asp Asn Lys Tyr Gln Glu Thr Leu Lys Glu Ile Asp
50 55 60

Asp Val Tyr Glu Lys Tyr Lys Lys Glu Asp Asp Leu Asn Gln Lys Lys
65 70 75 80

Arg Leu Gln Gln Leu Leu Gln Arg Ala Leu Ile Asn Ser Gln Glu Leu
85 90 95

Gly Asp Glu Lys Ile Gln Ile Val Thr Gln Met Leu Glu Leu Val Glu
100 105 110

Asn Arg Ala Arg Gln Met Glu Leu His Ser Gln Cys Phe Gln Asp Pro
115 120 125

Ala Glu Ser Glu Arg Ala Ser Asp Lys Ala Lys Met Asp Ser Ser Gln
130 135 140

Pro Glu Arg Ser Ser Arg Arg Pro Arg Arg Gln Arg Thr Ser Glu Ser
145 150 155 160

Arg Asp Leu Cys His Met Ala Asn Gly Ile Glu Asp Cys Asp Asp Gln
165 170 175

Pro Pro Lys Glu Lys Lys Ser Lys Ser Ala Lys Lys Lys Lys Arg Ser
180 185 190

Lys Ala Lys Gln Glu Arg Glu Ala Ser Pro Val Glu Phe Ala Ile Asp
195 200 205

Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu
210 215 220

Met Ile Gly Cys Asp Asn Glu Gln Cys Pro Ile Glu Trp Phe His Phe
225 230 235 240

Ser Cys Val Ser Leu Thr Tyr Lys Pro Lys Gly Lys Trp Tyr Cys Pro
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Thr Lys Lys Asp Arg Arg Ser Arg
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<400> 5

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20 25 30

Gln Asn Ala Met Asp Gln Leu Glu Gln Arg Val Ser Glu Phe Phe Met
35 40 45

Asn Ala Lys Lys Asn Lys Pro Glu Trp Arg Glu Glu Gln Met Ala Ser
50 55 60

Ile Lys Lys Asp Tyr Tyr Lys Ala Leu Glu Asp Ala Asp Glu Lys Val
65 70 75 80

Gln Leu Ala Asn Gln Ile Tyr Asp Leu Val Asp Arg His Leu Arg Lys
85 90 95

Leu Asp Gln Glu Leu Ala Lys Phe Lys Met Glu Leu Glu Ala Asp Asn
100 105 110

Ala Gly Ile Thr Glu Ile Leu Glu Arg Arg Ser Leu Glu Leu Asp Thr
115 120 125

Pro Ser Gln Pro Val Asn Asn His His Ala His Ser His Thr Pro Val
130 135 140

Glu Lys Arg Lys Tyr Asn Pro Thr Ser His His Thr Thr Thr Asp His
145 150 155 160

Ile Pro Glu Lys Lys Phe Lys Ser Glu Ala Leu Leu Ser Thr Leu Thr
165 170 175

Ser Asp Ala Ser Lys Glu Asn Thr Leu Gly Cys Arg Asn Asn Asn Ser
180 185 190

Thr Ala Ser Ser Asn Asn Ala Tyr Asn Val Asn Ser Ser Gln Pro Leu
195 200 205

Gly Ser Tyr Asn Ile Gly Ser Leu Ser Ser Gly Thr Gly Ala Gly Ala
210 215 220

Ile Thr Met Ala Ala Ala Gln Ala Val Gln Ala Thr Ala Gln Met Lys
225 230 235 240

Glu Gly Arg Arg Thr Ser Ser Leu Lys Ala Ser Tyr Glu Ala Phe Lys
245 250 255

Asn Asn Asp Phe Gln Leu Gly Lys Glu Phe Ser Met Ala Arg Glu Thr
260 265 270

Val Gly Tyr Ser Ser Ser Ser Ala Leu Met Thr Thr Leu Thr Gln Asn
275 280 285

Ala Ser Ser Ser Ala Ala Asp Ser Arg Ser Gly Arg Lys Ser Lys Asn
290 295 300

Asn Asn Lys Ser Ser Ser Gln Gln Ser Ser Ser Ser Ser Ser Ser
305 310 315 320

Ser Leu Ser Ser Cys Ser Ser Ser Ser Thr Val Val Gln Glu Ile Ser
325 330 335

Gln Gln Thr Thr Val Val Pro Glu Ser Asp Ser Asn Ser Gln Val Asp
340 345 350

Trp Thr Tyr Asp Pro Asn Glu Pro Arg Tyr Cys Ile Cys Asn Gln Val
355 360 365

Ser Tyr Gly Glu Met Val Gly Cys Asp Asn Gln Asp Cys Pro Ile Glu
370 375 380

Trp Phe His Tyr Gly Cys Val Gly Leu Thr Glu Ala Pro Lys Gly Lys
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Trp Tyr Cys Pro Gln Cys Thr Ala Ala Met Lys Arg Arg Gly Ser Arg
405 410 415

His Lys

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<213> Homo sapiens

<400> 6

Met Ala Ala Gly Met Tyr Leu Glu His Tyr Leu Asp Ser Ile Glu Asn
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20 25 30

Gln Arg Thr Glu Asp Leu Lys Ala Glu Ile Asp Lys Leu Ala Thr Glu
35 40 45

Tyr Met Ser Ser Ala Arg Ser Leu Ser Ser Glu Glu Lys Leu Ala Leu
50 55 60

Leu Lys Gln Ile Gln Glu Ala Tyr Gly Lys Cys Lys Glu Phe Gly Asp
65 70 75 80

Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val Asp Lys His
85 90 95

Ile Arg Arg Leu Asp Thr Asp Leu Ala Arg Phe Glu Ala Asp Leu Lys
100 105 110

Glu Lys Gln Ile Glu Ser Ser Asp Tyr Asp Ser Ser Ser Ser Lys Gly
115 120 125

Lys Lys Lys Gly Arg Thr Gln Lys Glu Lys Lys Ala Ala Arg Ala Arg
130 135 140

Ser Lys Gly Lys Asn Ser Asp Glu Glu Ala Pro Lys Thr Ala Gln Lys
145 150 155 160

Lys Leu Lys Leu Val Arg Thr Ser Pro Glu Tyr Gly Met Pro Ser Val
165 170 175

Thr Phe Gly Ser Val His Pro Ser Asp Val Leu Asp Met Pro Val Asp
180 185 190

Pro Asn Glu Pro Thr Tyr Cys Leu Cys His Gln Val Ser Tyr Gly Glu
195 200 205

Met Ile Gly Cys Asp Asn Pro Asp Cys Ser Ile Glu Trp Phe His Phe
210 215 220

Ala Cys Val Gly Leu Thr Thr Lys Pro Arg Gly Lys Trp Phe Cys Pro
225 230 235 240

Arg Cys Ser Gln Glu Arg Lys Lys Lys
245